

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Nathans et al., Jeremy
- (ii) TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR HOMOLOGOUS FACTORS (FHF's) AND METHODS OF USE
- (iii) NUMBER OF SEQUENCES: 37
- (iv) CORRESPONDENCE ADDRESS:
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  - (C) CITY: La Jolla
  - (D) STATE: CA
  - (E) COUNTRY: USA
  - (F) ZIP: 92037
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 08/705,245
  - (B) FILING DATE: 30-AUG-1996
  - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
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(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 243 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: not relevant
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Ala Ala Ala Ile Ala Ser Ser Leu Ile Arg Gln Lys Arg Gln Ala  
1                      5                      10                      15  
Arg Glu Ser Asn Ser Asp Arg Val Ser Ala Ser Lys Arg Arg Ser Ser  
20                      25                      30

Pro Ser Lys Asp Gly Arg Ser Leu Cys Glu Arg His Val Leu Gly Val  
 35 40 45  
 Phe Ser Lys Val Arg Phe Cys Ser Gly Arg Lys Arg Pro Val Arg Arg  
 50 55 60  
 Arg Pro Glu Pro Gln Leu Lys Gly Ile Val Thr Arg Leu Phe Ser Gln  
 65 70 75 80  
 Gln Gly Tyr Phe Leu Gln Met His Pro Asp Gly Thr Ile Asp Gly Thr  
 85 90 95  
 Lys Asp Glu Asn Ser Asp Tyr Thr Leu Phe Asn Leu Ile Pro Val Gly  
 100 105 110  
 Leu Arg Val Val Ala Ile Gln Gly Val Lys Ala Ser Leu Tyr Val Ala  
 115 120 125  
 Met Asn Gly Glu Gly Tyr Leu Tyr Ser Ser Asp Val Phe Thr Pro Glu  
 130 135 140  
 Cys Lys Phe Lys Glu Ser Val Phe Glu Asn Tyr Tyr Val Ile Tyr Ser  
 145 150 155 160  
 Ser Thr Leu Tyr Arg Gln Gln Glu Ser Gly Arg Ala Trp Phe Leu Gly  
 165 170 175  
 Leu Asn Lys Glu Gly Gln Ile Met Lys Gly Asn Arg Val Lys Lys Ile  
 180 185 190  
 Lys Pro Ser Ser His Phe Val Pro Lys Pro Ile Glu Val Cys Met Tyr  
 195 200 205  
 Arg Glu Pro Ser Leu His Glu Ile Gly Glu Lys Gln Gly Arg Ser Arg  
 210 215 220  
 Lys Ser Ser Gly Thr Pro Thr Met Asn Gly Gly Lys Val Val Asn Gln  
 225 230 235 240  
 Asp Ser Thr

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 245 amino acids
- (B) TYPE: amino acid.
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ala Ala Ala Ile Ala Ser Ser Leu Ile Arg Gln Lys Arg Gln Ala  
 1 5 10 15  
 Arg Glu Arg Glu Lys Ser Asn Ala Cys Lys Cys Val Ser Ser Pro Ser  
 20 25 30

Lys Gly Lys Thr Ser Cys Asp Lys Asn Lys Leu Asn Val Phe Ser Arg  
 35 40 45  
 Val Lys Leu Phe Gly Ser Lys Lys Arg Arg Arg Arg Arg Pro Glu Pro  
 50 55 60  
 Gln Leu Lys Gly Ile Val Thr Lys Leu Tyr Ser Arg Gln Gly Tyr His  
 65 70 75 80  
 Leu Gln Leu Gln Ala Asp Gly Thr Ile Asp Gly Thr Lys Asp Glu Asp  
 85 90 95  
 Ser Thr Tyr Thr Leu Phe Asn Leu Ile Pro Val Gly Leu Arg Val Val  
 100 105 110  
 Ala Ile Gln Gly Val Gln Thr Lys Leu Tyr Leu Ala Met Asn Ser Glu  
 115 120 125  
 Gly Tyr Leu Tyr Ile Ser Glu Leu Phe Thr Pro Glu Cys Lys Phe Lys  
 130 135 140  
 Glu Ser Val Phe Glu Asn Tyr Tyr Val Ile Tyr Ser Ser Met Ile Tyr  
 145 150 155 160  
 Arg Gln Gln Gln Ser Gly Arg Gly Trp Tyr Leu Gly Leu Asn Lys Glu  
 165 170 175  
 Gly Glu Ile Met Lys Gly Asn His Val Lys Lys Asn Lys Pro Ala Ala  
 180 185 190  
 His Phe Leu Pro Lys Pro Leu Lys Val Ala Met Tyr Lys Glu Pro Ser  
 195 200 205  
 Leu His Asp Leu Thr Glu Phe Ser Arg Ser Gly Ser Gly Thr Pro Thr  
 210 215 220  
 Lys Ser Arg Ser Val Ser Gly Val Leu Asn Gly Gly Lys Ser Met Ser  
 225 230 235 240  
 His Asn Glu Ser Thr  
 245

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Ala Ala Leu Ala Ser Ser Leu Ile Arg Gln Lys Arg Glu Val Arg  
 1 5 10 15  
 Glu Pro Gly Gly Ser Arg Pro Val Ser Ala Gln Arg Arg Val Cys Pro  
 20 25 30

Arg Gly Thr Lys Ser Leu Cys Gln Lys Gln Leu Leu Ile Leu Ile Ser  
 35 40 45  
 Lys Val Arg Leu Cys Gly Gly Arg Pro Ala Arg Pro Asp Arg Gly Pro  
 50 55 60  
 Glu Pro Gln Leu Lys Gly Ile Val Thr Lys Leu Phe Cys Arg Gln Gly  
 65 70 75 80  
 Phe Tyr Leu Gln Ala Asn Pro Asp Gly Thr Ile Asp Gly Thr Lys Asp  
 85 90 95  
 Glu Asn Ser Ser Phe Thr His Phe Asn Leu Ile Pro Val Gly Leu Arg  
 100 105 110  
 Val Val Ile Ile Gln Ser Ala Lys Leu Gly His Tyr Met Ala Met Asn  
 115 120 125  
 Ala Glu Gly Leu Asp Tyr Ser Ser Pro His Phe Thr Ala Glu Cys Arg  
 130 135 140  
 Phe Lys Glu Cys Val Phe Glu Asn Tyr Tyr Val Leu Tyr Ala Ser Ala  
 145 150 155 160  
 Leu Tyr Arg Gln Arg Arg Ser Gly Arg Ala Trp Tyr Leu Gly Leu Asp  
 165 170 175  
 Lys Glu Gly Gln Val Met Lys Gly Asn Arg Val Lys Lys Ile Lys Ala  
 180 185 190  
 Ala Ala His Phe Leu Pro Lys Leu Leu Glu Val Ala Met Tyr Gln Glu  
 195 200 205  
 Pro Ser Leu His Ser Val Pro Glu Ala Ser Pro Ser Ser Pro Pro Ala  
 210 215 220  
 Pro  
 225

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 247 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Ala Ala Ala Ile Ala Ser Gly Leu Ile Arg Gln Lys Arg Gln Ala  
 1 5 10 15  
 Arg Glu Gln His Trp Asp Arg Pro Ser Ala Ser Arg Arg Ser Ser  
 20 25 30  
 Pro Ser Lys Asn Arg Gly Leu Cys Asn Gly Asn Leu Val Asp Ile Phe  
 35 40 45

Ser Lys Val Arg Ile Phe Gly Leu Lys Lys Arg Arg Leu Arg Arg Gln  
 50 55 60  
 Asp Pro Gln Leu Lys Gly Ile Val Thr Arg Leu Tyr Cys Arg Gln Gly  
 65 70 75 80  
 Tyr Tyr Leu Gln Met His Pro Asp Gly Ala Leu Asp Gly Thr Lys Asp  
 85 90 95  
 Asp Ser Thr Asn Ser Thr Leu Phe Asn Leu Ile Pro Val Gly Leu Arg  
 100 105 110  
 Val Val Ala Ile Gln Gly Val Lys Thr Gly Leu Tyr Ile Ala Met Asn  
 115 120 125  
 Gly Glu Gly Tyr Leu Tyr Pro Ser Glu Leu Phe Thr Pro Glu Cys Lys  
 130 135 140  
 Phe Lys Glu Ser Val Phe Glu Asn Tyr Tyr Val Ile Tyr Ser Ser Met  
 145 150 155 160  
 Leu Tyr Arg Gln Gln Glu Ser Gly Arg Ala Trp Phe Leu Gly Leu Asn  
 165 170 175  
 Lys Glu Gly Gln Ala Met Lys Gly Asn Arg Val Lys Lys Ile Lys Pro  
 180 185 190  
 Ala Ala His Phe Leu Pro Lys Pro Leu Glu Val Ala Met Tyr Arg Glu  
 195 200 205  
 Pro Ser Leu His Asp Val Gly Glu Thr Val Pro Lys Pro Gly Val Thr  
 210 215 220  
 Pro Ser Lys Ser Thr Ser Ala Ser Ala Ile Met Asn Gly Gly Lys Pro  
 225 230 235 240  
 Val Asn Lys Ser Lys Thr Thr  
 245

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Ala Glu Gly Glu Ile Thr Thr Phe Thr Ala Leu Thr Glu Lys Phe  
 1 5 10 15  
 Asn Leu Pro Pro Gly Asn Tyr Lys Lys Pro Lys Leu Leu Tyr Cys Ser  
 20 25 30  
 Asn Gly Gly His Phe Leu Arg Ile Leu Pro Asp Gly Thr Val Asp Gly  
 35 40 45

Thr Arg Asp Arg Ser Asp Gln His Ile Gln Leu Gln Leu Ser Ala Glu  
 50 55 60  
 Ser Val Gly Glu Val Tyr Ile Lys Ser Thr Glu Thr Gly Gln Tyr Leu  
 65 70 75 80  
 Ala Met Asp Thr Asp Gly Leu Leu Tyr Gly Ser Gln Thr Pro Asn Glu  
 85 90 95  
 Glu Cys Leu Phe Leu Glu Arg Leu Glu Glu Asn His Tyr Asn Thr Tyr  
 100 105 110  
 Ile Ser Lys Lys His Ala Glu Lys Asn Trp Phe Val Gly Leu Lys Lys  
 115 120 125  
 Asn Gly Ser Cys Lys Arg Gly Pro Arg Thr His Tyr Gly Gln Lys Ala  
 130 135 140  
 Ile Leu Phe Leu Pro Leu Pro Val Ser Ser Asp  
 145 150 155

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids.
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Ala Ala Gly Ser Ile Thr Thr Leu Pro Ala Leu Pro Glu Asp Gly  
 1 5 10 15  
 Gly Ser Gly Ala Phe Pro Pro Gly His Phe Lys Asp Pro Lys Arg Leu  
 20 25 30  
 Tyr Cys Lys Asn Gly Gly Phe Phe Leu Arg Ile His Pro Asp Gly Arg  
 35 40 45  
 Val Asp Gly Val Arg Glu Lys Ser Asp Pro His Ile Lys Leu Gln Leu  
 50 55 60  
 Gln Ala Glu Glu Arg Gly Val Val Ser Ile Lys Gly Val Cys Ala Asn  
 65 70 75 80  
 Arg Tyr Leu Ala Met Lys Glu Asp Gly Arg Leu Leu Ala Ser Lys Cys  
 85 90 95  
 Val Thr Asp Glu Cys Phe Phe Phe Glu Arg Leu Glu Ser Asn Asn Tyr  
 100 105 110  
 Asn Thr Tyr Arg Ser Arg Lys Tyr Thr Ser Trp Tyr Val Ala Leu Lys  
 115 120 125

Arg Thr Gly Gln Tyr Lys Leu Gly Ser Lys Thr Gly Pro Gly Gln Lys  
130 135 140

Ala Ile Leu Phe Leu Pro Met Ser Ala Lys Ser  
145 150 155

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Ala Pro Leu Gly Glu Val Gly Asn Tyr Phe Gly Val Gln Asp Ala  
1 5 10 15  
Val Pro Phe Gly Asn Val Pro Val Leu Pro Val Asp Ser Pro Val Leu  
20 25 30  
Leu Ser Asp His Leu Gly Gln Ser Glu Ala Gly Gly Leu Pro Arg Gly  
35 40 45  
Pro Ala Val Thr Asp Leu Asp His Leu Lys Gly Ile Leu Arg Arg Arg  
50 55 60  
Gln Leu Tyr Cys Arg Thr Gly Phe His Leu Glu Ile Phe Pro Asn Gly  
65 70 75 80  
Thr Ile Gln Gly Thr Arg Lys Asp His Ser Arg Phe Gly Ile Leu Glu  
85 90 95  
Phe Ile Ser Ile Ala Val Gly Leu Val Ser Ile Arg Gly Val Asp Ser  
100 105 110  
Gly Leu Tyr Leu Gly Met Asn Glu Lys Gly Glu Leu Tyr Gly Ser Glu  
115 120 125  
Lys Leu Thr Gln Glu Cys Val Phe Arg Glu Gln Phe Glu Glu Asn Trp  
130 135 140  
Tyr Asn Thr Tyr Ser Ser Asn Leu Tyr Lys His Val Asp Thr Gly Arg  
145 150 155 160  
Arg Tyr Tyr Val Ala Leu Asn Lys Asp Gly Thr Pro Arg Glu Gly Thr  
165 170 175  
Arg Thr Lys Arg His Gln Lys Phe Thr His Phe Leu Pro Arg Pro Val  
180 185 190  
Asp Pro Asp Lys Val Pro Glu Leu Tyr Lys Asp Ile Leu Ser Gln Ser  
195 200 205

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 243 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Ala Ala Ala Ile Ala Ser Ser Leu Ile Arg Gln Lys Arg Gln Ala  
1 5 10 15  
Arg Glu Ser Asn Ser Asp Arg Val Ser Ala Ser Lys Arg Arg Ser Ser  
20 25 30  
Pro Ser Lys Asp Gly Arg Ser Leu Cys Glu Arg His Val Leu Gly Val  
35 40 45  
Phe Ser Lys Val Arg Phe Cys Ser Gly Arg Lys Arg Pro Val Arg Arg  
50 55 60  
Arg Pro Glu Pro Gln Leu Lys Gly Ile Val Thr Arg Leu Phe Ser Gln  
65 70 75 80  
Gln Gly Tyr Phe Leu Glu Met His Pro Asp Gly Thr Ile Asp Gly Thr  
85 90 95  
Lys Asp Glu Asn Ser Asp Tyr Thr Leu Phe Asn Leu Ile Pro Val Gly  
100 105 110  
Leu Arg Val Val Ala Ile Gln Gly Val Lys Ala Ser Leu Tyr Val Ala  
115 120 125  
Met Asn Gly Glu Gly Tyr Leu Tyr Ser Ser Asp Val Phe Thr Pro Glu  
130 135 140  
Cys Lys Phe Lys Glu Ser Val Phe Glu Asn Tyr Tyr Val Ile Tyr Ser  
145 150 155 160  
Ser Thr Leu Tyr Arg Gln Gln Glu Ser Gly Arg Ala Trp Glu Leu Gly  
165 170 175  
Leu Asn Lys Glu Gly Gln Ile Met Lys Gly Asn Arg Val Lys Lys Thr  
180 185 190  
Lys Pro Ser Ser His Phe Val Pro Lys Pro Ile Glu Val Cys Met Tyr  
195 200 205  
Arg Glu Pro Ser Leu His Glu Ile Gly Glu Lys Gln Gly Arg Ser Arg  
210 215 220  
Lys Ser Ser Gly Thr Pro Thr Met Asn Gly Gly Lys Val Val Asn Gln  
225 230 235 240  
Asp Ser Thr



(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 245 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: not relevant

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Thr Ala Ala Ile Ala Ser Ser Leu Ile Arg Gln Lys Arg Gln Ala  
1 5 10 15

Arg Glu Arg Glu Lys Ser Asn Ala Cys Lys Cys Val Ser Ser Pro Ser  
20 25 30

Lys Gly Lys Thr Ser Cys Asp Lys Asn Lys Leu Asn Val Phe Ser Arg  
35 40 45

Val Lys Leu Phe Gly Ser Lys Lys Arg Arg Arg Arg Arg Pro Glu Pro  
50 55 60

Gln Leu Lys Gly Ile Val Thr Lys Leu Tyr Ser Arg Gln Gly Tyr His  
65 70 75 80

Leu Gln Leu Gln Ala Asp Gly Thr Ile Asp Gly Thr Lys Asp Glu Asp  
85 90 95

Ser Thr Tyr Thr Leu Phe Asn Leu Ile Pro Val Gly Leu Arg Val Val  
100 105 110

Ala Ile Gln Gly Val Gln Thr Lys Leu Tyr Leu Ala Met Asn Ser Glu  
115 120 125

Gly Tyr Leu Tyr Thr Ser Glu His Phe Thr Pro Glu Cys Lys Phe Lys  
130 135 140

Glu Ser Val Phe Glu Asn Tyr Tyr Val Thr Tyr Ser Ser Met Ile Tyr  
145 150 155 160

Arg Gln Gln Gln Ser Gly Arg Gly Trp Tyr Leu Gly Leu Asn Lys Glu  
165 170 175

Gly Glu Ile. Met Lys Gly Asn His Val Lys Lys Asn Lys Pro Ala Ala  
180 185 190

His Phe Leu Pro Lys Pro Leu Lys Val Ala Met Tyr Lys Glu Pro Ser  
195 200 205

Leu His Asp Leu Thr Glu Phe Ser Arg Ser Gly Ser Gly Thr Pro Thr  
210 215 220

Lys Ser Arg Ser Val Ser Gly Val Leu Asn Gly Gly Lys Ser Met Ser  
225 230 235 240

His Asn Glu Ser Thr  
245

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Ala Ala Leu Ala Ser Ser Leu Ile Arg Gln Lys Arg Glu Val Arg  
1 5 10 15  
Glu Pro Gly Gly Ser Arg Pro Val Ser Ala Gln Arg Arg Val Cys Pro  
20 25 30  
Arg Gly Thr Lys Ser Leu Cys Gln Lys Gln Leu Leu Ile Leu Leu Ser  
35 40 45  
Lys Val Arg Leu Cys Gly Gly Arg Pro Thr Arg Gln Asp Arg Gly Pro  
50 55 60  
Glu Pro Gln Leu Lys Gly Ile Val Thr Lys Leu Phe Cys Arg Gln Gly  
65 70 75 80  
Phe Tyr Leu Gln Ala Asn Pro Asp Gly Ser Ile Gln Gly Thr Pro Glu  
85 90 95  
Asp Thr Ser Ser Phe Thr His Phe Asn Leu Ile Pro Val Gly Leu Arg  
100 105 110  
Val Val Thr Ile Gln Ser Ala Lys Leu Gly His Tyr Met Ala Met Asn  
115 120 125  
Ala Glu Gly Leu Leu Tyr Ser Ser Pro His Phe Thr Ala Glu Cys Arg  
130 135 140  
Phe Lys Glu Cys Val Phe Glu Asn Tyr Tyr Val Leu Tyr Ala Ser Ala  
145 150 155 160  
Leu Tyr Arg Gln Arg Arg Ser Gly Arg Ala Trp Tyr Leu Gly Leu Asp  
165 170 175  
Lys Glu Gly Arg Val Met Lys Gly Asn Arg Val Lys Lys Thr Lys Ala  
180 185 190  
Ala Ala His Phe Val Pro Lys Leu Leu Glu Val Ala Met Tyr Arg Glu  
195 200 205  
Pro Ser Leu His Ser Val Pro Glu Thr Ser Pro Ser Ser Pro Pro Ala  
210 215 220  
His  
225

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 247 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Ala Ala Ala Ile Ala Ser Gly Leu Ile Arg Gln Lys Arg Gln Ala  
1 5 10 15  
Arg Glu Gln His Trp Asp Arg Pro Ser Ala Ser Arg Arg Arg Ser Ser  
20 25 30  
Pro Ser Lys Asn Arg Gly Leu Phe Asn Gly Asn Leu Val Asp Ile Phe  
35 40 45  
Ser Lys Val Arg Ile Phe Gly Leu Lys Lys Arg Arg Leu Arg Arg Gln  
50 55 60  
Asp Pro Gln Leu Lys Gly Ile Val Thr Arg Leu Tyr Cys Arg Gln Gly  
65 70 75 80  
Tyr Tyr Leu Gln Met His Pro Asp Gly Ala Leu Asp Gly Thr Lys Asp  
85 90 95  
Asp Ser Thr Asn Ser Thr Leu Phe Asn Leu Ile Pro Val Gly Leu Arg  
100 105 110  
Val Val Ala Ile Gln Gly Val Lys Thr Gly Leu Tyr Ile Ala Met Asn  
115 120 125  
Gly Glu Gly Tyr Leu Tyr Pro Ser Glu Leu Phe Thr Pro Glu Cys Lys  
130 135 140  
Phe Lys Glu Ser Val Phe Glu Asn Tyr Tyr Val Ile Tyr Ser Ser Met  
145 150 155 160  
Leu Tyr Arg Gln Gln Glu Ser Gly Arg Ala Trp Phe Leu Gly Leu Asn  
165 170 175  
Lys Glu Gly Gln Val Met Lys Gly Asn Arg Val Lys Lys Thr Lys Pro  
180 185 190  
Ala Ala His Phe Leu Pro Lys Pro Leu Glu Val Ala Met Tyr Arg Glu  
195 200 205  
Pro Ser Leu His Asp Val Gly Glu Thr Val Pro Lys Ala Gly Val Thr  
210 215 220  
Pro Ser Lys Ser Thr Ser Ala Ser Ala Ile Met Asn Gly Gly Lys Pro  
225 230 235 240  
Val Asn Lys Cys Lys Thr Thr  
245

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 245 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: not relevant  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEO ID NO:12:

[illegible]

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 206 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met	Ser	Gly	Pro	Gly	Thr	Ala	Ala	Val	Ala	Leu	Leu	Pro	Ala	Val	Leu	
1				5				10						15		
Leu	Ala	Leu	Leu	Ala	Pro	Trp	Ala	Gly	Arg	Gly	Gly	Ala	Ala	Ala	Pro	
			20					25					30			
Thr	Ala	Pro	Asn	Gly	Thr	Leu	Glu	Ala	Glu	Leu	Glu	Arg	Arg	Trp	Glu	
			35				40					45				
Ser	Leu	Val	Ala	Leu	Ser	Leu	Ala	Arg	Leu	Pro	Val	Ala	Ala	Gln	Pro	
	50					55				60						
Lys	Glu	Ala	Ala	Val	Gln	Ser	Gly	Ala	Gly	Asp	Tyr	Leu	Leu	Gly	Ile	
65					70					75					80	
Lys	Arg	Leu	Arg	Arg	Leu	Tyr	Cys	Asn	Val	Gly	Ile	Gly	Phe	His	Glu	
				85					90					95		
Gln	Ala	Leu	Pro	Asp	Gly	Arg	Ile	Gly	Gly	Ala	His	Ala	Asp	Thr	Arg	
			100					105					110			
Asp	Ser	Leu	Leu	Glu	Leu	Ser	Pro	Val	Glu	Arg	Gly	Val	Val	Ser	Ile	
		115					120					125				
Phe	Gly	Val	Ala	Ser	Arg	Phe	Phe	Val	Ala	Met	Ser	Ser	Lys	Gly	Lys	
	130					135					140					
Leu	Tyr	Gly	Ser	Pro	Phe	Phe	Thr	Asp	Glu	Cys	Ile	Phe	Lys	Glu	Ile	
145					150					155					160	
Leu	Leu	Pro	Asn	Asn	Tyr	Asn	Ala	Tyr	Glu	Ser	Tyr	Lys	Tyr	Pro	Gly	
				165					170					175		
Met	Glu	Ile	Ala	Leu	Ser	Lys	Asn	Gly	Lys	Thr	Lys	Lys	Gly	Asn	Arg	
			180					185					190			
Val	Ser	Pro	Thr	Met	Lys	Val	Thr	His	Phe	Leu	Pro	Arg	Leu			
		195					200					205				

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 268 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met Ser Leu Ser Phe Leu Leu Leu Leu Phe Phe Ser His Leu Ile Leu  
1 5 10 15  
Ser Ala Trp Ala His Gly Glu Lys Arg Leu Ala Pro Lys Gly Gln Pro  
20 25 30  
Gly Pro Ala Ala Thr Asp Arg Asn Pro Ile Asp Ser Ser Arg Gln  
35 40 45  
Ser Ser Ser Ser Ala Met Ser Ser Ser Ser Ala Ser Ser Ser Pro Ala  
50 55 60  
Ala Ser Leu Gly Ser Gln Gly Ser Gly Leu Glu Gln Ser Ser Phe Gln  
65 70 75 80  
Trp Ser Pro Ser Gly Arg Arg Thr Gly Ser Leu Tyr Cys Arg Val Gly  
85 90 95  
Ile Gly Phe His Leu Gln Ile Tyr Pro Asp Gly Lys Val Asn Gly Ser  
100 105 110  
His Glu Ala Asn Met Leu Ser Val Leu Glu Ile Phe Ala Val Ser Gln  
115 120 125  
Gly Ile Val Gly Ile Arg Gly Val Phe Ser Asn Lys Phe Leu Ala Met  
130 135 140  
Ser Lys Lys Gly Lys Leu His Ala Ser Ala Lys Phe Thr Asp Asp Cys  
145 150 155 160  
Lys Phe Arg Glu Arg Phe Gln Glu Asn Ser Tyr Asn Thr Tyr Ala Ser  
165 170 175  
Ala Ile His Arg Thr Glu Lys Thr Gly Arg Glu Trp Tyr Val Ala Leu  
180 185 190  
Asn Lys Pro Gly Lys Ala Lys Arg Gly Cys Ser Pro Arg Val Lys Pro  
195 200 205  
Gln His Ile Ser Thr His Phe Leu Pro Arg Phe Lys Gln Ser Glu Gln  
210 215 220  
Pro Glu Leu Ser Phe Thr Val Thr Val Pro Glu Lys Lys Asn Pro Pro  
225 230 235 240  
Ser Pro Ile Lys Ser Lys Ile Pro Leu Ser Ala Pro Arg Lys Asn Thr  
245 250 255  
Asn Ser Val Lys Tyr Arg Leu Lys Phe Arg Phe Gly  
260 265

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Met Ser Arg Gly Ala Gly Arg Leu Gln Gly Thr Leu Trp Ala Leu Val  
1 5 10 15  
Phe Leu Gly Ile Leu Val Gly Met Val Val Pro Ser Pro Ala Gly Thr  
20 25 30  
Arg Ala Asn Asn Thr Leu Leu Asp Ser Arg Gly Trp Gly Thr Leu Leu  
35 40 45  
Ser Arg Ser Arg Ala Gly Leu Ala Gly Glu Ile Ala Gly Val Asn Trp  
50 55 60  
Glu Ser Gly Tyr Leu Val Gly Ile Lys Arg Gln Arg Arg Leu Tyr Cys  
65 70 75 80  
Asn Val Gly Ile Gly Phe His Glu Gln Val Leu Pro Asp Gly Arg Ile  
85 90 95  
Ser Gly Thr His Glu Glu Asn Pro Tyr Ser Leu Leu Glu Ile Ser Thr  
100 105 110  
Val Glu Arg Gly Val Val Ser Leu Phe Gly Val Arg Ser Ala Leu Glu  
115 120 125  
Val Ala Met Asn Ser Lys Gly Arg Leu Tyr Ala Thr Pro Ser Phe Gln  
130 135 140  
Glu Glu Cys Lys Phe Arg Glu Thr Leu Leu Pro Asn Asn Tyr Asn Ala  
145 150 155 160  
Tyr Glu Ser Asp Leu Tyr Gln Gly Thr Tyr Ile Ala Leu Ser Lys Tyr  
165 170 175  
Gly Arg Val Lys Arg Gly Ser Lys Val Ser Pro Ile Met Thr Val Thr  
180 185 190  
His Phe Leu Pro Arg Ile  
195

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 194 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Met His Lys Trp Ile Leu Thr Trp Ile Leu Pro Thr Leu Leu Tyr Arg  
1 5 10 15  
Ser Cys Phe His Ile Ile Cys Leu Val Gly Thr Ile Ser Leu Ala Cys  
20 25 30

Asn Asp Met Thr Pro Glu Gln Met Ala Thr Asn Val Asn Cys Ser Ser  
 35 40 45  
 Pro Glu Arg His Thr Arg Ser Tyr Asp Tyr Met Glu Gly Gly Asp Ile  
 50 55 60  
 Arg Val Arg Arg Leu Phe Cys Arg Thr Gln Trp Tyr Leu Arg Ile Asp  
 65 70 75 80  
 Lys Arg Gly Lys Val Lys Gly Thr Gln Glu Met Lys Asn Asn Tyr Asn  
 85 90 95  
 Ile Met Glu Ile Arg Thr Val Ala Val Gly Ile Val Ala Ile Lys Gly  
 100 105 110  
 Val Glu Ser Glu Phe Leu Tyr Ala Met Asn Lys Glu Gly Lys Leu Tyr  
 115 120 125  
 Ala Lys Lys Glu Cys Asn Glu Asp Cys Asn Phe Lys Glu Leu Ile Leu  
 130 135 140  
 Glu Asn His Tyr Asn Thr Tyr Ala Ser Ala Lys Trp Thr His Asn Gly  
 145 150 155 160  
 Gly Glu Met Phe Val Ala Leu Asn Gln Lys Gly Ile Pro Val Arg Gly  
 165 170 175  
 Lys Lys Thr Lys Lys Glu Gln Lys Thr Ala His Phe Leu Pro Met Ala  
 180 185 190  
 Ile Thr

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 215 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Met Gly Ser Pro Arg Ser Ala Leu Ser Cys Leu Leu Leu His Leu Leu  
 1 5 10 15  
 Val Leu Cys Leu Gln Ala Gln Val Thr Val Gln Ser Ser Pro Asn Phe  
 20 25 30  
 Thr Gln His Val Arg Glu Gln Ser Leu Val Thr Asp Gln Leu Ser Arg  
 35 40 45  
 Arg Leu Ile Arg Thr Tyr Gln Leu Tyr Ser Arg Thr Ser Gly Lys His  
 50 55 60  
 Val Gln Val Leu Ala Asn Lys Arg Ile Asn Ala Met Ala Glu Asp Gly  
 65 70 75 80



Asp	Pro	Phe	Ala	Lys	Leu	Ile	Val	Glu	Thr	Asp	Thr	Phe	Gly	Ser	Arg	
				85					90					95		
Val	Arg	Val	Arg	Gly	Ala	Glu	Thr	Gly	Leu	Tyr	Ile	Cys	Met	Asn	Lys	
			100					105					110			
Lys	Gly	Lys	Leu	Ile	Ala	Lys	Ser	Asn	Gly	Lys	Gly	Lys	Asp	Cys	Val	
		115					120					125				
Phe	Ile	Glu	Ile	Val	Leu	Glu	Asn	Asn	Tyr	Thr	Ala	Leu	Gln	Asn	Ala	
	130					135					140					
Lys	Tyr	Glu	Gly	Trp	Tyr	Met	Ala	Phe	Thr	Arg	Lys	Gly	Arg	Pro	Arg	
145					150					155					160	
Lys	Gly	Ser	Lys	Thr	Arg	Gln	His	Gln	Arg	Glu	Val	His	Phe	Met	Lys	
				165					170					175		
Arg	Leu	Pro	Arg	Gly	His	His	Thr	Thr	Glu	Gln	Ser	Leu	Arg	Phe	Glu	
			180					185						190		
Phe	Leu	Asn	Tyr	Pro	Pro	Phe	Thr	Arg	Ser	Leu	Arg	Gly	Ser	Gln	Arg	
		195					200					205				
Thr	Trp	Ala	Pro	Glu	Pro	Arg										
	210					215										

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1422 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GAATTCGCA CACTGCGTTC GGGGTACCAA GTGGAAGGGG AAGAACGATG CCCAAAATAA	60
CAAGACGTGC CTGGGACCGC CCCGCCCCGC CCCCCGGCCG CCAGAGGTTG GGGAAGTTTA	120
CATCTGGATT TTCACACATT TTGTCGCCAC TGCCCAGACT TTGACTAACC TTGTGAGCGC	180
CGGGTTTTTCG ATACTGCAGC CTCCTCAAAT TTTAGCACTG CCTCCCCGCG ACTGCCCTTT	240
CCCTGGCCGC CCAGGTCCTG CCCTCGCCCC GCGCGAGCGC AAGCCGGAGG GCGCAGTAGA	300
GGCTGGGGCC TGAGGCCCTC GCTGAGCAGC TATGGCTGCG GCGATAGCCA GCTCCTTGAT	360
CCGGCAGAAG CGGCAGGCGA GGGAGTCCAA CAGCGACCGA GTGTCGGCCT CCAAGCGCCG	420
CTCCAGCCCC AGCAAAGACG GCGCTCCCT GTGCGAGAGG CACGTCCTCG GGGTGTTCAG	480
CAAAGTGCGC TTCTGCAGCG GCCGCAAGAG GCCGGTGAGG CGGAGACCAG AACCCAGCT	540
CAAAGGGATT GTGACAAGGT TATTCAGCCA GCAGGGATAC TTCCTGCAGA TGCACCCAGA	600
TGGTACCATT GATGGGACCA AGGACGAAAA CAGCGACTAC ACTCTCTTCA ATCTAATTCC	660
CGTGGGCCTG CGTGTAGTGG CCATCCAAGG AGTGAAGGCT AGCCTCTATG TGGCCATGAA	720

TGGTGAAGGC TATCTCTACA GTTCAGATGT TTTCACTCCA GAATGCAAAT TCAAGGAATC	780
TGTGTTTGAA AACTACTATG TGATCTATTC TTCCACACTG TACCGCCAGC AAGAATCAGG	840
CCGAGCTTGG TTTCTGGGAC TCAATAAAGA AGGTCAAATT ATGAAGGGGA ACAGAGTGAA	900
GAAAACCAAG CCCTCATCAC ATTTTGTACC GAAACCTATT GAAGTGTGTA TGTACAGAGA	960
ACCATCGCTA CATGAAATTG GAGAAAAACA AGGGCGTTCA AGGAAAAGTT CTGGAACACC	1020
AACCATGAAT GGAGGCAAAG TTGTGAATCA AGATTCAACA TAGCTGAGAA CTCTCCCCTT	1080
CTTCCCTCTC TCATCCCTTC CCCTTCCCTT CCTTCCCATT TACCCATTTC CTTCCAGTAA	1140
ATCCACCCAA GGAGAGGAAA ATAAAATGAC AACGCAAGAC CTAGTGGCTA AGATTCTGCA	1200
CTCAAATCT TCCTTTGTGT AGGACAAGAA AATTGAACCA AAGCTTGCTT GTTGCAATGT	1260
GGTAGAAAAT TCACGTGCAC AAAGATTAGC ACACTTAAAA GCAAAGGAAA AAATAAATCA	1320
GAAGTCCATA AATATTAAAC TAAACTGTAT TGTATTAGT AGAAGGCTAA TTGTAATGAA	1380
GACATTAATA AAGATGAAAT AACTTATTA CTTTCGGAAT TC	1422

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1150 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

AATTCCGCTT GCACAGTGTC CGCCGGGCGC AGGGGCCGAC CGCACGAGT CGCGCAGTTC	60
TGCCTCCGCC TGCCAGTCTC GCCC GCGATC CCGGCCCGGG GCTGTGGCGT CGACTCCGAC	120
CCAGGCAGCC AGCAGCCCGC GCGGGAGCCG GACCGCCGCC GGAGGAGCTC GGACGGCATG	180
CTGAGCCCCC TCCTTGCTG AAGCCCGAGT GCGGAGAAGC CCGGGCAAAC GCAGGCTAAG	240
GAGACCAAAG CGGCGAAGTC GCGAGACAGC GGACAAGCAG CGGAGGAGAA GGAGGAGGAG	300
GCGAACCAG AGAGGGGCAG CAAAAGAAGC GGTGGTGGTG GCGTCGTGG CCATGGCGGC	360
GGCTATCGCC AGCTCGCTCA TCCGTCAGAA GAGGCAAGCC CGCGAGCGCG AGAAATCCAA	420
CGCCTGCAAG TGTGTCAGCA GCCCCAGCAA AGGCAAGACC AGCTGCGACA AAAACAAGTT	480
AAATGTCTTT TCCCGGGTCA AACTCTTCGG CTCCAAGAAG AGGCGCAGAA GAAGACCAGA	540
GCCTCAGCTT AAGGGTATAG TTACCAAGCT ATACAGCCGA CAAGGCTACC ACTTGCAGCT	600
GCAGGCGGAT GGAACCATTG ATGGCACCAA AGATGAGGAC AGCACTTACA CTCTGTTTAA	660
CCTCATCCCT GTGGGTCTGC GAGTGGTGGC TATCCAAGGA GTTCAAACCA AGCTGTACTT	720
GGCAATGAAC AGTGAGGGAT ACTTGATACAC CTCGGAAGTT TTCACACCTG AGTGCAAATT	780

CAAAGAATCA GTGTTTGAAA ATTATTATGT GACATATTCA TCAATGATAT ACCGTCAGCA	840
GCAGTCAGGC CGAGGGTGGT ATCTGGGTCT GAACAAAGAA GGAGAGATCA TGAAAGGCAA	900
CCATGTGAAG AAGAACAAGC CTGCAGCTCA TTTTCTGCCT AAACCACTGA AAGTGGCCAT	960
GTACAAGGAG CCATCACTGC ACGATCTCAC GGAGTTCTCC CGATCTGGAA GCGGGACCCC	1020
AACCAAGAGC AGAAGTGTCT CTGGCGTGCT GAACGGAGGC AAATCCATGA GCCACAATGA	1080
ATCAACGTAG CCAGTGAGGG CAAAAGAAGG GCTCTGTAAC AGAACCTTAC CTCCAGGTGC	1140
TGTTGAATTC	1150

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 961 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GAATTCCGGC TCTTGGGGAG CCCAGCGCGC TCCGGGCGCC TGCCGGTTTG GGGGTGTCTC	60
CTCCCGGGGC GCTATGGCGG CGCTGGCCAG TAGCCTGATC CGGCAGAAGC GGGAGGTCCG	120
CGAGCCCGGG GGCAGCCGGC CGGTGTCGGC GCAGCGGCGC GTGTGTCCCC GCGGCACCAA	180
GTCCCTTTGC CAGAAGCAGC TCCTCATCCT GCTGTCCAAG GTGCGACTGT GCGGGGGGCG	240
GCCCGCGCGG CCGGACCGCG GCCCGGAGCC TCAGCTCAAA GGCATCGTCA CCAAAGTGT	300
CTGCCGCCAG GGTTCCTACC TCCAGGCGAA TCCCGACGGA AGCATCCAGG GCACCCCA	360
GGATAACCAGC TCCTTCACCC ACTTCAACCT GATCCCTGTG GGCCTCCGTG TGGTCACCAT	420
CCAGAGCGCC AAGCTGGGTC ACTACATGGC CATGAATGCT GAGGGACTGC TCTACAGTTC	480
GCCGCATTTT ACAGCTGAGT GTCGCTTTAA GGAGTGTGTC TTTGAGAATT ACTACGTCCT	540
GTACGCCTCT GCTCTCTACC GCCAGCGTCG TTCTGGCCGG GCCTGGTACC TCGGCCTGGA	600
CAAGGAGGGC CAGGTCATGA AGGGAAACCG AGTTAAGAAG ACCAAGGCAG CTGCCCCACTT	660
TCTGCCCAAG CTCCTGGAGG TGGCCATGTA CCAGGAGCCT TCTCTCCACA GTGTCCCCGA	720
GGCCTCCCCCT TCCAGTCCCC CTGCCCCCTG AAATGTAGTC CCTGGACTGG AGGTTCCCTG	780
CACTCCCAGT GAGCCAGCCA CCACCACAAC CTGTCTCCCA GTCCTGCTCT CACCCCTGCT	840
GCCACACACA TGCCCTGAGC AGCCAGGTCC CACTAGGTGC TCTACCCTGA GGGAGCCTAG	900
GGGCTGACTG TGACTTCCGA GGCTGCTGAG ACCCTTAGAT CTTTGGGCCT AGGAGGGAGT	960
C	961

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 971 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CGCCGCCTTC CCCTCCGGTG CCCC CGGCTC GCCGTCTCTC CGCGCCCTCC CTCCCCGGAC	60
CCGTTCCCCG GGCCACCATG GCCGCGGCCA TCGCTAGCGG CTTGATCCGC CAGAAGCGGC	120
AGGCGCGGGA GCAGCACTGG GACCGGCCGT CTGCCAGCAG GAGGCGGAGC AGCCCCAGCA	180
AGAACC GCGG GCTCTGCAAC GGCAACCTGG TGGATATCTT CTCCAAAGTG CGCATCTTCG	240
GCCTCAAGAA GCGCAGGTTG CGGCGCCAAG ATCCCCAGCT CAAGGGTATA GTGACCAGGT	300
TATATTGCAG GCAAGGCTAC TACTTGCAAA TGCACCCCGA TGGAGCTCTC GATGGAACCA	360
AGGATGACAG CACTAATTCT ACACTCTTCA ACCTCATACC AGTGGGACTA CGTGTGTGTTG	420
CCATCCAGGG AGTGAAAACA GGGTTGTATA TAGCCATGAA TGGAGAAGGT TACCTCTACC	480
CATCAGAACT TTTTACCCCT GAATGCAAGT TTAAAGAATC TGTTTTTGAA AATTATTATG	540
TAATCTACTC ATCCATGTTG TACAGACAAC AGGAATCTGG TAGAGCCTGG TTTTGGGGAT	600
TAAATAAGGA AGGGCAAGCT ATGAAAGGGA ACAGAGTAAA GAAAACCAAA CCAGCAGCTC	660
ATTTTCTACC CAAGCCATTG GAAGTTGCCA TGTACCGAGA ACCATCTTTG CATGATGTTG	720
GGGAAACGGT CCCGAAGCCT GGGGTGACGC CAAGTAAAAG CACAAGTGCG TCTGCAATAA	780
TGAATGGAGG CAAACCAGTC AACAAGAGTA AGACAACATA GCCAGATCCT CACAGGTGTT	840
GTGACTTATT CGTCCTGAGC ACAGTTGAGT GATTTATCCT CACCAGACAT TCCTGCTCCG	900
TGGCTGAAGA GCAGCAGGAA GTAAGCTAAT GCTTATTCTT TGCTGTCTCC GAACTTCTCT	960
GTTGCAAGTG G	971

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE

- (D) OTHER INFORMATION: Xaa in position 4 is Isoleucine or Leucine;  
Xaa in position 7 is Serine or Glycine.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Ala Ala Ala Xaa Ala Ser Xaa Ser Leu Ile Arg Gln Lys Arg  
1 5 10

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in position 9 is Arginine or Lysine.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Pro Gln Leu Lys Gly Ile Val Thr Xaa  
1 5

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in position 2 is Leucine or Histidine.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Thr Xaa Phe Asn Leu Ile Pro Val Gly Leu Arg Val Val  
1 5 10

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in position 4 is Glycine, Serine, or Alanine; Xaa in position 7 is Tyrosine or Leucine.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Ala Met Asn Xaa Glu Gly Xaa Leu Tyr  
1 5

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE

- (D) OTHER INFORMATION: Xaa in position 3 is Serine or Cysteine.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Lys Glu Xaa Val Phe Glu Asn Tyr Tyr Val  
1                      5                      10

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Val Phe Glu Asn Tyr Tyr Val  
1                      5

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in position 4 is Alanine or Glycine;  
Xaa in position 6 is Phenylalanine or Tyrosine.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Ser Gly Arg Xaa Trp Xaa Leu Gly Leu  
1                      5

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 10 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: not relevant
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (ix) FEATURE:
  - (D) OTHER INFORMATION: Xaa in position 5 is Arginine or Histidine;  
Xaa in position 9 is Threonine or Asparagine.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Met Lys Gly Asn Xaa Val Lys Lys Xaa Lys  
1                    5                    10

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 7 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: not relevant
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (ix) FEATURE:
  - (D) OTHER INFORMATION: Xaa in position 5 is Histidine or Arginine.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Met Lys Gly Asn Xaa Val Lys  
1                    5

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 10 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: not relevant
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (ix) FEATURE:
  - (D) OTHER INFORMATION: Xaa in position 2 is Cysteine or Alanine;  
Xaa in position 5 is Arginine, Glutamine,  
or Lysine.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Val Xaa Met Tyr Xaa Glu Pro Ser Leu His  
1                    5                    10

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 30 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

GACGAGATAT TAGAATTCTA CTCGNNNNNN

30

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 33 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CCCCCCCCCG ACGAGATATT AGAATTCTAC TCG

33

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 32 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

CCGATCGAAT TCGTNTTYGA RAAYTAYTAY GT

32

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 32 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GCGATCGGAT CCTTNACRTG RTTNCCYTTC AT

32



(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 32 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

GCGATCGGAT CCTTNACYCT RTTNCCYTTC AT

32

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 32 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GCGATCGGAT CCTTNACNCG RTTNCCYTTC AT

32